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FIGURE 1-1

FIGURE 1-1
FIGURE 1-2
FIGURE 1-3
FIGURE 1-4
FIGURE 1-5

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-80      -60      -40
-28  AGTATTGTTGTCGTGTTGCCCTGTAGGGGTCATCCCTCAAGTGATCACTTAGTTCAA  31

-20      -1      20
32  GAGTCCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCCTTGCTGCTC  91
-8      M N T S H L L A L L
40      60      80
92  CCAAAATCTCCACAAGGTGAAACAGAAACCCCTGGGCACCCCATACAACTTCTCT  151
12  P K S P Q G E N R S K P L G T P Y N F S  31

100      120      140
152  GAACATTGCCAGGATTCCTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG  211
32  E H C Q D S V D V M V F I V T S Y S I E  51

160      180      200
212  ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCCTGATGTGTGACTGTGAGGCAGAAGGAG  271
52  T V V G V L G N L C L M C V T V R Q K E  71

```

FIGURE 1-2

220 240 260
272 AAAGCCAAACGTGACCAACCTGCTTATCGCCAAACCTGGCCTTCTCTGACTTCCTCATGTGC 331
72 K A N V T N L L I A N L A F S D F L M C 91

280 300 320
332 CTCCTCTGCCAGCCGCTGACCCGCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 391
92 L L C Q P L T A V Y T I M D Y W I F G E 111

340 360 380
392 ACCCTCTGCAAGATGTCGGCCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 451
112 T L C K M S A F I Q C M S V T V S I L S 131

400 420 440
452 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCAACCCAAACAGGCTGGAAGCCC 511
132 L V L V A L E R H Q L I I N P T G W K P 151

460 480 500
512 AGCATCTCACAGGCCCTACCTGGGGATTGTGCTCATCTGGGTCATTCGCTGTGCTCTCC 571
152 S I S Q A Y L G I V L I W V I A C V L S 171

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FIGURE 1-3

572	C T G C C C T T T C C T G G C C A A C A G C A T C C C T G G A G A A T G T C T T C C A C A A G A C C A C T C C C A A G G C T	520	540	560	631
172	L P F L A N S I L E N V F H K N H S K A				191
580		600	620		
632	C T G G A G T T C C T G G C A G A T A A G T G G T C T G T A C C G A G T C C T G G C C A C T G G C T C A C C A C C G C				691
192	L E F L A D K V V C T E S W P L A H H R				211
640		660	680		
692	A C C A T C T A C A C C A C C T T C C T G C T C C T C T T C C A G T A C T G C C T C C C A C T G G G C T T C A T C C T G				751
212	T I Y T T F L L L L F Q Y C L P L G F I L				231
700		720	740		
752	G T C T G T T A T G C A C G C A T C T A C C G G C C C T G C A G A G G C A G G G G C G T G T T C A C A A G G C				811
232	V C Y A R I Y R R L Q R Q R Q G R V F H K G				251
760		780	800		
812	A C C T A C A G C T T G C G A G C T G G G C A C A T G A A G C A G T C A A T G T G G T G C T G G T G G T G A T G T G				871
252	T Y S L R A G H M K Q V N V V L V V M V				271

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FIGURE 1-4

872	GTGGCC	820	840	860	
272	V A F A V L W L P L H V F N S L E D W H				931 291
		880	900	920	
932	CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTCCTTGCC				991 311
292	H E A I P I C H G N L I F L V C H L L A				
		940	960	980	
992	ATGGCCCTCCACCTGCGTCAACCCCATTCATCTATGGCTTTCTCAACACCACTTCAAGAAG				1051 331
312	M A S T C V N P F I Y G F L N T N F K K				
		1000	1020	1040	
1052	GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCTGGAGGAGTCGGAGCAT				1111 351
332	E I K A A L V L T C Q Q S A P L E E S E H				
		1060	1080	1100	
1112	CTGCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG				1171 371
352	L P L S T V H T E V S K G S L R L S G R				

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FIGURE 1-5

1120	1140	1160	
1172 TCCAATCCCATTTAAACCAGGCTAGGTCTTCTCCCTGCCATGTCCCTGCCAGGCTCTTC			1231
372 S N P I *			375
1180	1200	1220	
1232 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCACCCAGCATTCCTGGCTTCTG			1291

FIGURE 2-1
FIGURE 2-2
FIGURE 2-3

FIGURE 2-1

					50
1					
hp25a	MNTSHLLALL	LPKSPQGENR	SKPLGTPYNF	SEHCQDSVDV	MVFIVTSYSI
human Y1	MN.STLFSQV	ENHSHVSNFS	EKNAQLLAFE	NDDCHLPLAM	IFTLALAYGA
rat Y1	MN.STLFSRV	ENYSVHYNVS	E.NSPFLAFE	NDDCHLPLAV	IFTLALAYGA
mouse Y1	MN.STLFSKV	ENHSHIYNAS	E.NSPLLAFE	NDDCHLPLAV	IFTLALAYGA
51					100
hp25a	ETVVGVLGNL	CLMCVTVRQK	EKANVTNLLI	ANLAFSDFLM	CLLCQPLTAV
human Y1	VIIILGVSGNL	ALIIIIILKQK	EMRNVTNILI	VNLSFSDLLV	AIMCLPFTFV
rat Y1	VIIILGVSGNL	ALIIIIILKQK	EMRNVTNILI	VNLSFSDLLV	AVMCLPFTFV
mouse Y1	VIIILGVSGNL	ALIIIIILKQK	EMRNVTNILI	VNLSFSDLLV	AVMCLPFTFV
101					150
hp25a	YTIMDYWIFG	ETLCKMSAFI	QCMSVTVSIL	SLVLVALERH	QLIINPTGWK
human Y1	YTLMDHWVFG	EAMCKLNPV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR
rat Y1	YTLMDHWVFG	ETMCKLNPV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR
mouse Y1	YTLMDHWVFG	ETMCKLNPV	QCVSITVSIF	SLVLI AVERH	QLIINPRGWR
151					200
hp25a	PSISQAYLGI	VLIWVIACVL	SLPFLANSIL	ENVFHKNHSH	ALEFLADKV
human Y1	PNNRHAYVGI	AVIWWLAVAS	SLPFLIYQVM	TDEPFQNV	.LDAYKDKYV
rat Y1	PNNRHAYIGI	TVIWWLAVAS	SLPFLVIYQIL	TDEPFQNV	.LAAFKDKYV
mouse Y1	PNNRHAYIGI	TVIWWLAVAS	SLPFLVIYQIL	TDEPFQNV	.LAAFKDKYV

FIGURE 2-2

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FIGURE 2-3

hp25a	351	388
human Y1	EHLPLSTVHT EVSKGSLRLS GRSNPI*... ..	
rat Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKINN NDDNEKI*	
mouse Y1	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM N.DNEKI*	
	ETIAMSTMHT DVSKTSLKQA SPVAFKKISM N.DNEKV*	

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FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

-170 -150 -130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110 -90 -70

TTCTTACCTGGTTCCATTTTACATGCCTGGACCTTTGAGTTCCATTTGTTTGTTCAG

-50 -30 -10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG

M

10 30 50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCTCTACAAGGTAAGAATGGGACC

N T S H L M A S L S P A F L Q G K N G T

70 90 110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCGGCAGATCTGTTG

N P L D S L Y N L S D G C Q D S A D L L

130 150 170

GCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGGGGTCCTAGGAAACCTCTGC

A F I I T T Y S V E T V L G V L G N L C

190 210 230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC

L I F V T T R Q K E K S N V T N L L I A

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FIGURE 3-2

250 270 290
AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC
N L A F S D F L M C L I C Q P L T V T Y

310 330 350
ACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAAGATGTTAACGTTTCATCCAG
T I M D Y W I F G E V L C K M L T F I Q

370 390 410
TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCTGGAGAGGCACCAG
C M S V T V S I L S L V L V A L E R H Q

430 450 470
CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCAGGCCTACCTGGGGATTGTG
L I I N P T G W K P S I S Q A Y L G I V

490 510 530
GTCATCTGGTTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCTGGCCAATAGCATCCTGAAC
V I W F I S C F L S L P F L A N S I L N

550 570 590
GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCTGGAAGACAAGGTTGTCTGC
D L F H Y N H S K V V E F L E D K V V C

610 630 650
TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC
F V S W S S D H H R L I Y T T F L L L F

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FIGURE 3-3

570 690 710
CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG
Q Y C V P L A F I L V C Y M R I Y Q R L

730 750 770
CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG
Q R Q R R A F H T H T C S S R V G Q M K

790 810 830
CGGATCAATGGCATGCTCATGGCAATGGTGA CTGCCTTTGCAGTTCTCTGGCTGCCCCTG
R I N G M L M A M V T A F A V L W L P L

850 870 890
CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC
H V F N T L E D W Y Q E A I P A C H G N

910 930 950
CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTTCATC
L I F L M C H L F A M A S T C V N P F I

970 990 1010
TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT
Y G F L N I N F K K D I K A L V L T C R

1030 1050 1070
TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC
C R P P Q G E P E P L P L S T V H T D L

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FIGURE 3-4

1090

1110

1130

TCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCATGTAGTCATGTCTAGGCTCT
S K G S M R M G S K S N V M *

1150

1170

1190

TCCGCCATTTTCTTTTCGACACACCCTTTCACTGAGCTAAGTAGACACAATGCAAGCTGTG

1210

1230

1250

GTATCATCCTGCCATTTCTGGTCTTTGGGGCCCAGACAGGCGGCAAGAGACTTGAAGCTT

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FIGURE 4

1 50

Y4rat MNTSHLMASL SPAFLQGKNG TNPLDSLNL SDGCQDSADL LAPIITTYSV
Y4hum MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI

51 100

— I — II —

Y4rat ETVLGVLGNL CLIFVTTRQK EKSNTNLLI ANLAFSDFLM CLICQPLTVT
Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLLCQPLTAV

101 150

— III —

Y4rat YTIMDYWIFG EVLCKMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK
Y4hum YTIMDYWIFG ETLCKMSAPI QCMSVTVSIL SLVLVALERH QLIINPTGWK

151 200

— IV —

Y4rat PSISQAYLGI VVIWFISCFL SLPFLANSIL NDLFHYNHSH VVEFLEDKVV
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKHSH ALEFLADKVV

201 250

— V —

Y4rat CFVSWSSDHH RLIYTTFLLL PQYCVPLAFI LVCYMRIYQR LQRQRAFHT
Y4hum CTESWPLAHH RTIYTTFLLL PQYCLPLGFI LVCYARIYRR LQRQGRVPHK

251 300

— VI —

Y4rat HTCSSRVGQM KRINGMLMAM VTAPAVLWLP LHVFNLTLEDW YQEAIPACHG
Y4hum GTYSLRAGHM KQNVVLVVM VVAFVAVLWLP LHVFNLSLEDW HHEAIPICHG

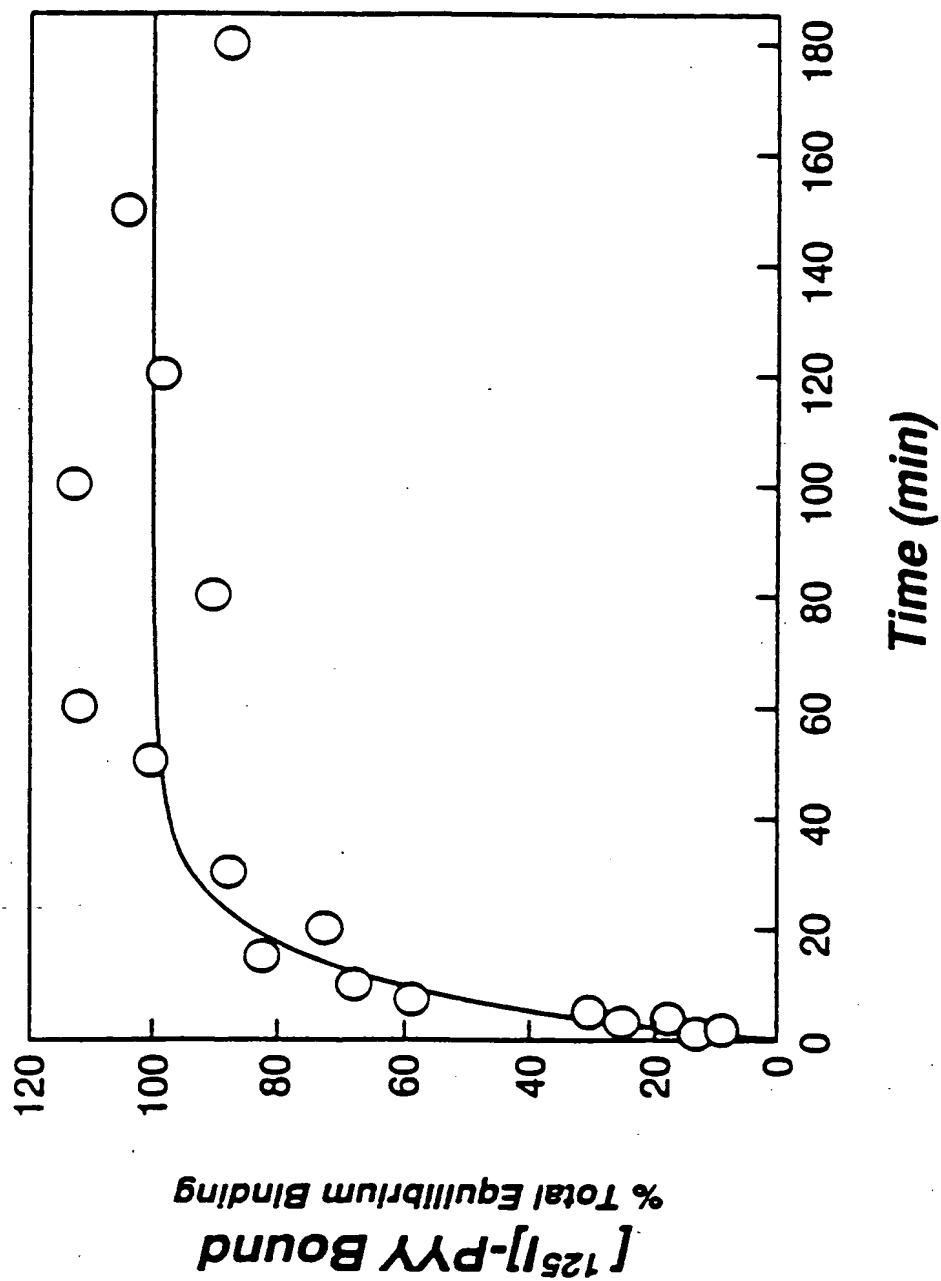
301 350

— VII —

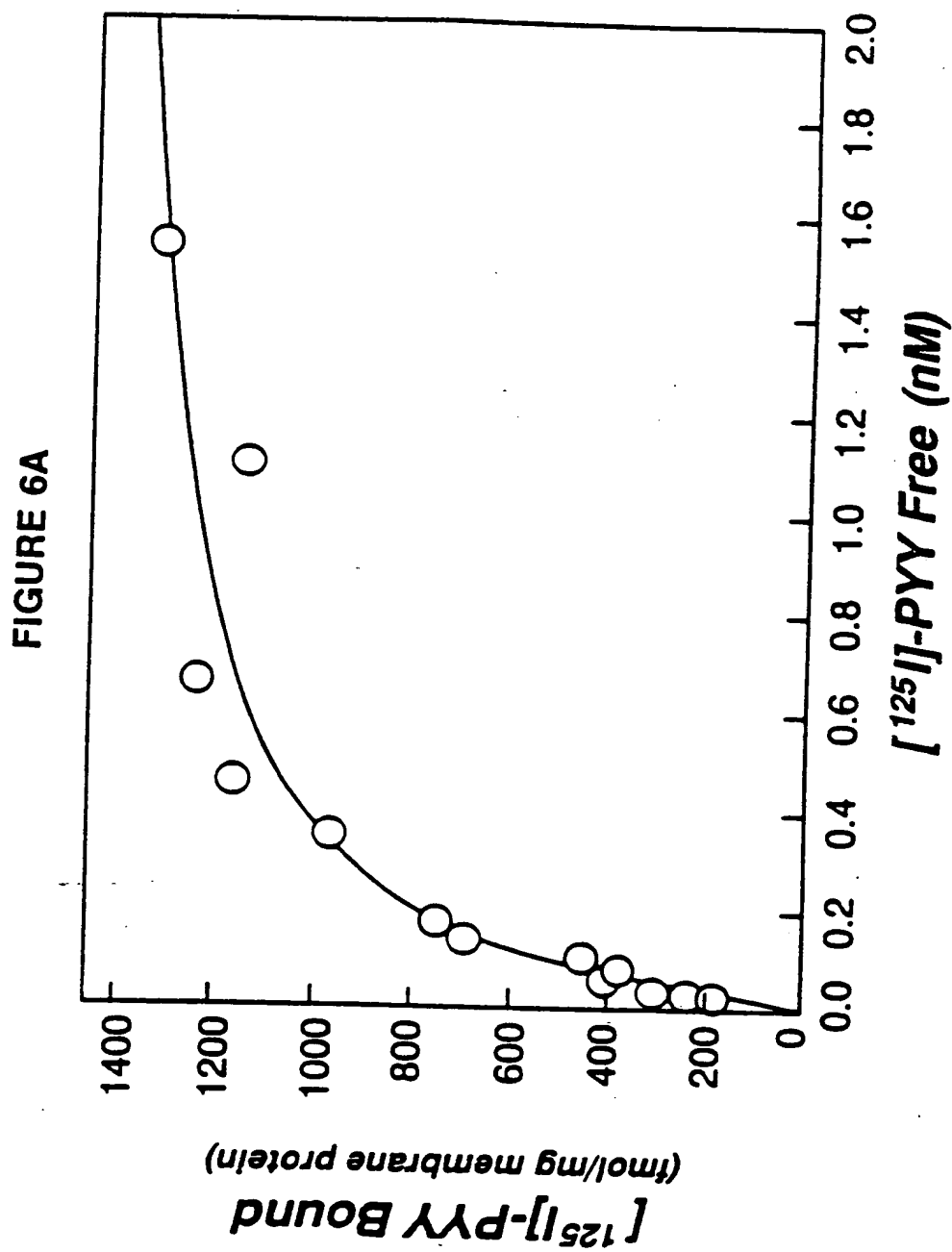
Y4rat NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTG RCRPPQGEPE
Y4hum NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KEIKALVLTG QQSAPLEESE

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FIGURE 5

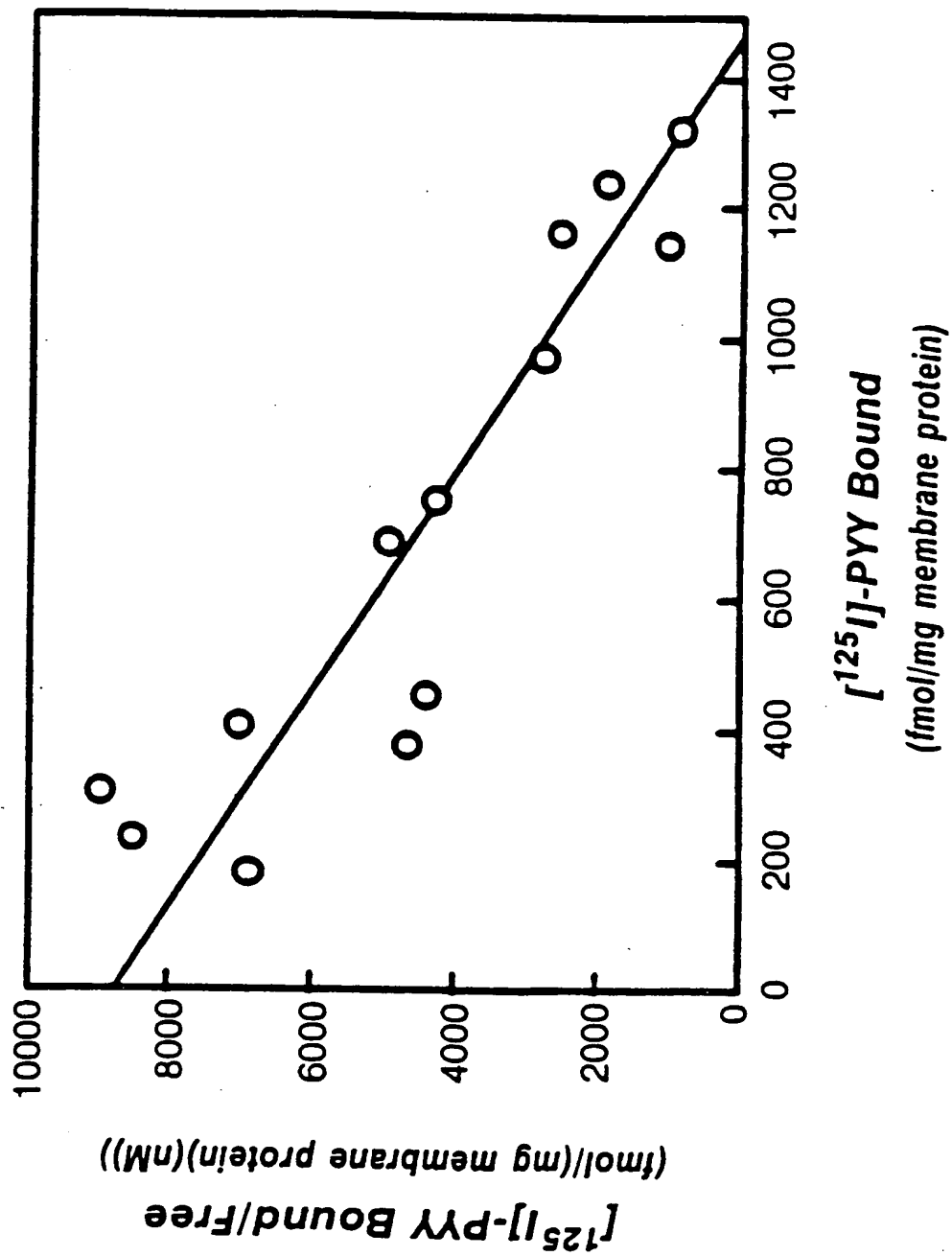


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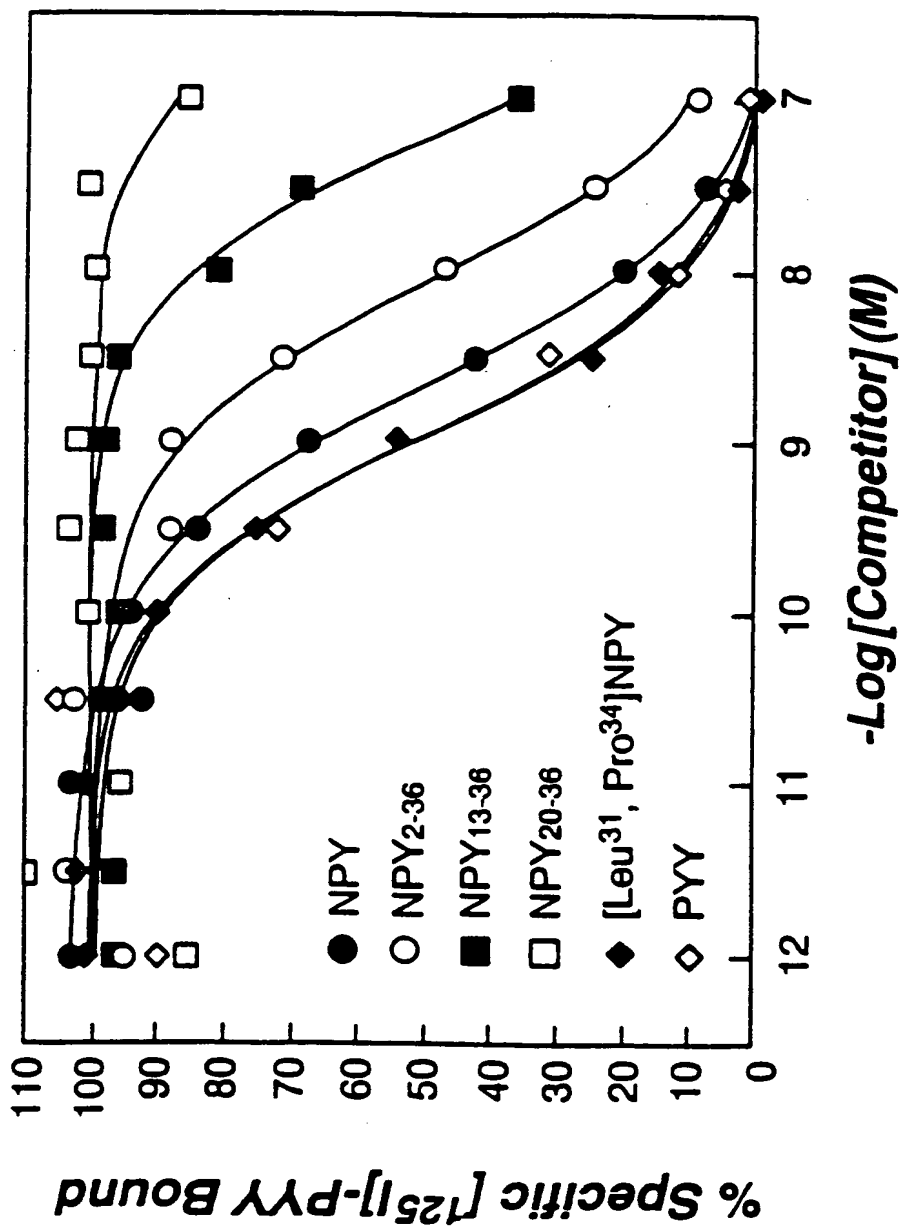
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FIGURE 6B



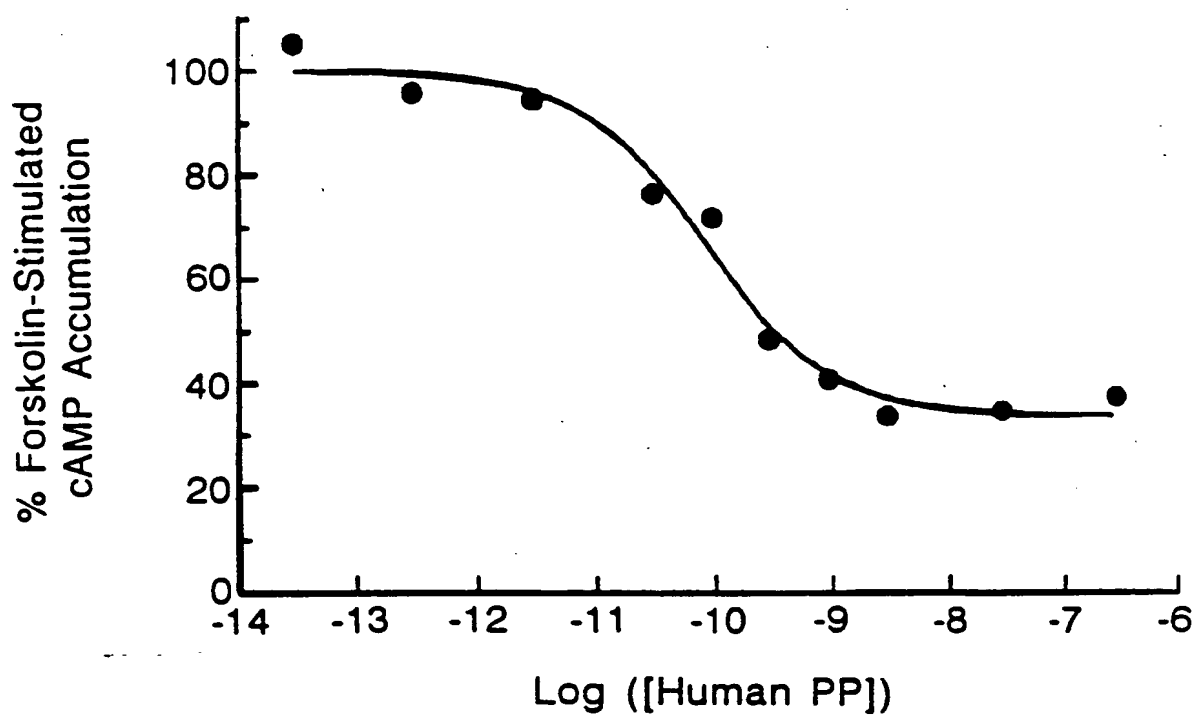
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FIGURE 7



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FIGURE 8



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FIGURE 9A

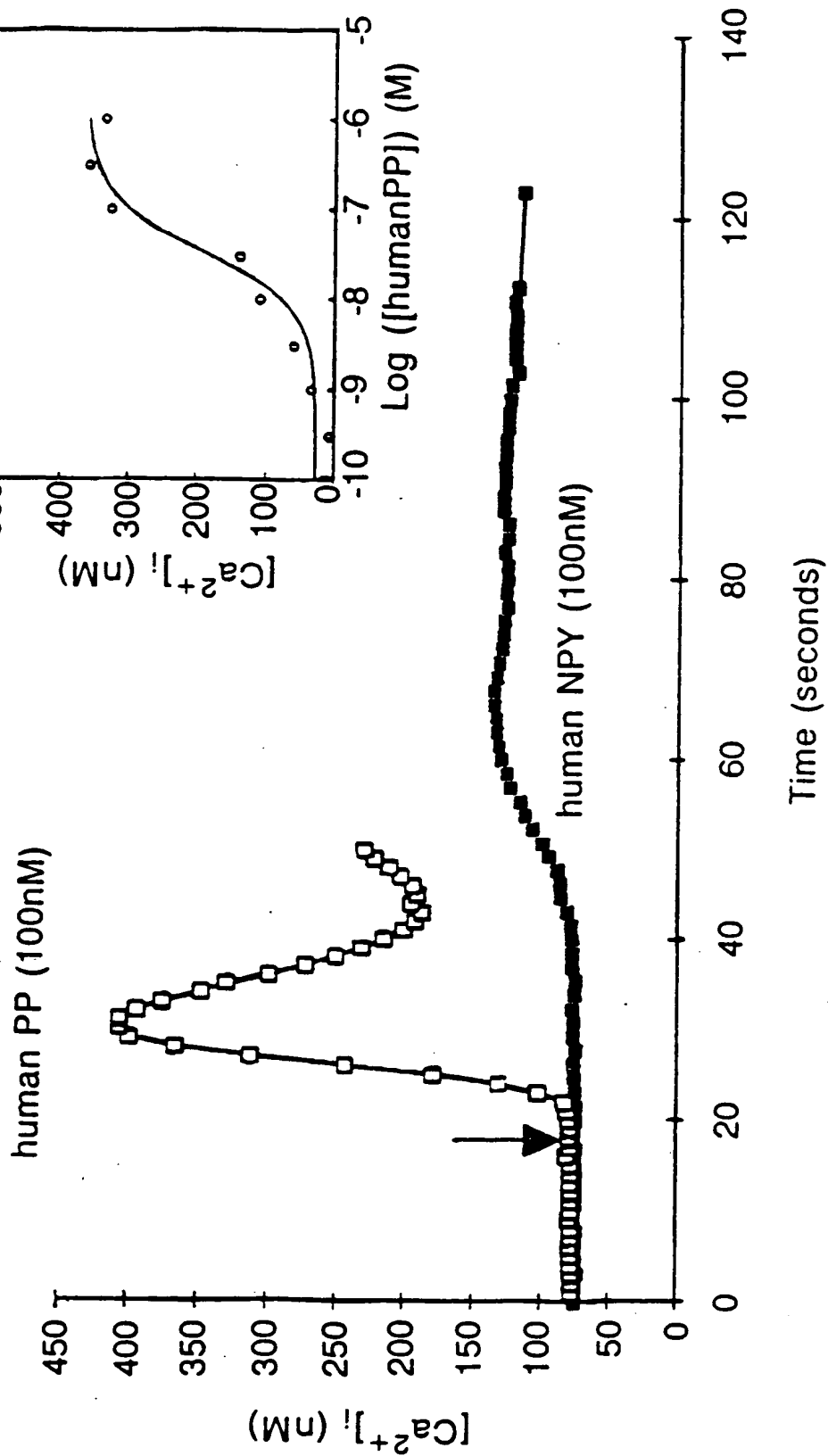


FIGURE 9B

